BIOTECH. .OGY
SYSTEMS
BRANCH

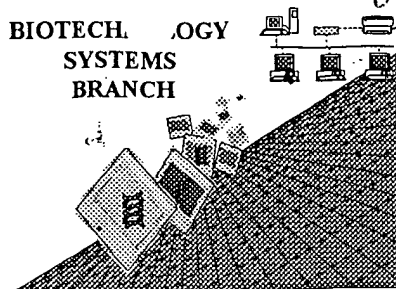# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 09/883,848

Source: O/PE

Date Processed by STIC: 10/12/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/883,848_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

· 2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 10/12/2001
PATENT APPLICATION: US/09/883,848   TIME: 12:14:38

Input Set : A:\CIBT-P01-119 Seq List.txt
Output Set: N:\CRF3\10122001\I883848.raw

Does Not Comply
Corrected Diskette Needed

```
   3 <110> APPLICANT: Ling, L.
   4         Sanicola-Nadel, M.
   6 <120> TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES
   8 <130> FILE REFERENCE: CIBT-P01-119
  10 <140> CURRENT APPLICATION NUMBER: 09/883,848
  11 <141> CURRENT FILING DATE: 2001-09-24
  13 <150> PRIOR APPLICATION NUMBER: 60/211,919
  14 <151> PRIOR FILING DATE: 2000-06-16
  16 <160> NUMBER OF SEQ ID NOS: 48
  18 <170> SOFTWARE: PatentIn Ver. 2.1
```

ERRORED SEQUENCES

```
 167 <210> SEQ ID NO: 6
 168 <211> LENGTH: 1425
 169 <212> TYPE: DNA
 170 <213> ORGANISM: Homo sapiens
 172 <400> SEQUENCE: 6
 173 atgctgctgc tggcgagatg tctgctgcta gtcctcgtct cctcgctgct ggtatgctcg 60
 174 ggactggcgt gcggaccggg caggggggttc gggaagagga ggcaccccaa aaagctgacc 120
 175 cctttagcct acaagcagtt tatccccaat gtggccgaga agaccctagg cgccagcgga 180
 176 aggtatgaag ggaagatctc cagaaactcc gagcgattta aggaactcac ccccaattac 240
 177 aaccccgaca tcatatttaa ggatgaagaa aacaccggag cggacaggct gatgactcag 300
 178 aggtgtaagg acaagttgaa cgctttggcc atctcggtga tgaaccagtg gccaggagtg 360
 179 aaactgcggg tgaccgaggg ctgggacgaa gatggccacc actcagagga gtctctgcac 420
 180 tacgagggcc gcgcagtgga catcaccacg tctgaccgcg accgcagcaa gtacggcatg 480
 181 ctggcccgcc tggcggtgga ggccggcttc gactgggtgt actacgagtc caaggcacat 540
 182 atccactgct cggtgaaagc agagaactcg gtggcggcca aatcgggagg ctgcttcccg 600
 183 ggctcggcca cggtgcacct ggagcagggc ggcaccaagc tggtgaagga cctgagcccc 660
 184 ggggaccgcg tgctggcggc ggacgaccag ggccggctgc tctacagcga cttcctcact 720
 185 ttcctggacc gcgacgacgg cgccaagaag gtcttctacg tgatcgagac gcgggagccg 780
 186 cgcgagcgcc tgctgctcac cgccgcgcac ctgctctttg tggcgccgca caacgactcg 840
 187 gccaccgggg agcccgaggc gtcctcgggc tcggggccgc cttccggggg cgcactgggg 900
 188 cctcgggcgc tgttcgccag ccgcgtgcgc ccgggccagc gcgtgtacgt ggtggccgag 960
 189 cgtgacgggg accgccggct cctgcccgcc gctgtgcaca gcgtgaccct aagcgaggag 1020
 190 gccgcgggcg cctacgcgcc gctcacggcc caggcacca ttctcatcaa ccgggtgctg 1080
 191 gcctcgtgct acgcggtcat cgaggagcac agctgggcgc accgggcctt cgcgcccttc 1140
 192 cgcctggcgc acgcgctcct ggctgcactg gcgcccgcgc gcacggaccg cggcggggac 1200
 193 agcggcggcg gggaccgcgg gggcggcggc ggcagagtag ccctaaccgc tccaggtgct 1260
 194 gccgacgctc cgggtgcggg ggccaccgcg ggcatccact ggtactcgca gctgctctac 1320
 195 caaataggca cctggctcct ggacagcgag gccctgcacc cgctgggcat ggcggtcaag 1380
 196 tccagcnnna gccggggggc cggggggaggg gcgcgggagg gggcc 1425
 728 <210> SEQ ID NO: 15
 729 <211> LENGTH: 475
 730 <212> TYPE: PRT
 731 <213> ORGANISM: Homo sapiens
```

```
733 <400> SEQUENCE: 15
734 Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
735  1                   5                  10                  15
737 Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
738             20                  25                  30
740 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
741         35                  40                  45
743 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
744     50                  55                  60
746 Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
747 65                  70                  75                  80
749 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
750                 85                  90                  95
752 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
753             100                 105                 110
755 Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
756             115                 120                 125
758 Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
759     130                 135                 140
761 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
762 145                 150                 155                 160
764 Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
765             165                 170                 175
767 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
768             180                 185                 190
770 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
771         195                 200                 205
773 Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
774         210                 215                 220
776 Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
777 225                 230                 235                 240
779 Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
780             245                 250                 255
782 Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
783             260                 265                 270
785 Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
786         275                 280                 285
788 Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
789         290                 295                 300
791 Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
792 305                 310                 315                 320
794 Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
795             325                 330                 335
797 Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
798         340                 345                 350
800 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
801         355                 360                 365
803 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
804         370                 375                 380
```

RAW SEQUENCE LISTING   DATE: 10/12/2001
PATENT APPLICATION: US/09/883,848   TIME: 12:14:38

Input Set : A:\CIBT-P01-119 Seq List.txt
Output Set: N:\CRF3\10122001\I883848.raw

```
      806 Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
      807 385                 390                 395                 400
      809 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Arg Val Ala Leu Thr
      810             405                 410                 415
      812 Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
      813             420                 425                 430
      815 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
      816             435                 440                 445
E-->  818 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
      819         450                 455                 460
      821 Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
      822 465                 470                 475
     1348 <210> SEQ ID NO: 23
     1349 <211> LENGTH: (174) /75 shown
     1350 <212> TYPE: PRT
     1351 <213> ORGANISM: Homo sapiens
     1353 <400> SEQUENCE: 23
     1354 Cys Gly Pro Gly Arg Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys
     1355   1               5                 10                  15
     1357 Leu Val Pro Leu Ala Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys
     1358             20                  25                  30
     1360 Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser
     1361             35                  40                  45
     1363 Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe
     1364         50                  55                  60
     1366 Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys
     1367  65                  70                  75                  80
     1369 Lys Asp Arg Leu Asn Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro
     1370             85                  90                  95
     1372 Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His
     1373             100                 105                 110
     1375 Ser Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr
     1376         115                 120                 125
     1378 Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val
     1379         130                 135                 140
     1381 Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Val His
     1382 145                 150                 155                 160
     1384 Cys Ser Val Lys Ser Glu His Ser Ala Ala Ala Lys Thr Gly Gly
E--> 1385             165                 170                 175
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 10/12/2001
PATENT APPLICATION: US/09/883,848   TIME: 12:14:39

Input Set : **A:\CIBT-P01-119 Seq List.txt**
Output Set: **N:\CRF3\10122001\I883848.raw**

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:196 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:818 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:1385 M:252 E: No. of Seq. differs, <211>LENGTH:Input:174 Found:175 SEQ:23
L:1698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1714 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26